

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER

(ii) TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
10 PROTEINS IN PLANTS AND THEIR USES

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
20 (E) COUNTRY: U.S.A.
(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1

30 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE:
35 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

40 Prior applications total,
including application
described below: 1

45 U.S. Patent Application Serial No. 08/367,395
Filed 12/30/94
Docket No. 210/152

100-433660

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 34,613
(C) REFERENCE/DOCKET NUMBER: 212/127

(ix) TELECOMMUNICATION INFORMATION:

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2025-12-12 10:10:10

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 3517 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

15 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 124....2445

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCCGGGGTT ACGGGCTGGC CAGCAGGCTG TGCCCCGAG TCCGGTCAGCAGGAGGGGAA 60
 GAAGTGGCCT AAAATCTCTC CCGCATCGGC AGCCCAGGCC TAGTGCCCTA CCAGCCACCA 120
 25 GCC ATG GCT CTC TTC TTG CTC ACC TGC CTG CTG GCT GTC TTT TCA GCG 168
 Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala
 1 5 10 15
 30 GCC ACG GCA CAA AGC TCC TTA TTG GGT CCC AGC TCC ATA TTT GGT CCC 216
 Ala Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro
 20 25 30
 35 GGG GAG GTG AAT GTT TTG GAA GGC GAC TCG GTG TCC ATC ACA TGC TAC 264
 Gly Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
 35 40 45
 40 TAC CCA ACA ACC TCC GTC ACC CGG CAC AGC CGG AAG TTC TGG TGC CGG 312
 Tyr Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg
 50 55 60
 45 GAA GAG GAG AGC GGC CGC TGC GTG ACG CTT GCC TCG ACC GGC TAC ACG 360
 Glu Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr
 65 70 75
 50 TCC CAG GAA TAC TCC GGG AGA GGC AAG CTC ACC GAC TTC CCT GAT AAA 408
 Ser Gln Glu Tyr Ser Ser Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys
 80 85 90 95
 55 GGG GAG TTT GTG GTG ACT GTT GAC CAA CTC ACC CAG AAC GAC TCA GGG 456
 Gly Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly
 100 105 110
 60 AGC TAC AAG TGT GGC GTG GGA GTC AAC GGC CGT GGC CTG GAC TTC GGT 504
 Ser Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly
 115 120 125
 65 GTC AAC GTG CTG GTC AGC CAG AAG CCA GAG CCT GAT GAC GTT GTT TAC 552
 Val Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr
 130 135 140
 AAA CAA TAT GAG AGT TAT ACA GTA ACC ATC ACC TGC CCT TTC ACA TAT 600
 Lys Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr
 145 150 155
 GCG ACT AGG CAA CTA AAG AAG TCC TTT TAC AAG GTG GAA GAC GGG GAA 648

	Ala	Thr	Arg	Gln	Leu	Lys	Ser	Phe	Tyr	Lys	Val	Glu	Asp	Gly	Glu		
	160					165				170					175		
5	CTT	GTA	CTC	ATC	ATT	GAT	TCC	AGC	AGT	AAG	GAG	GCA	AAG	GAC	CCC	AGG	696
	Leu	Val	Leu	Ile	Ile	Asp	Ser	Ser	Ser	Lys	Glu	Ala	Lys	Asp	Pro	Arg	
					180					185					190		
10	TAT	AAG	GGC	AGA	ATA	ACG	TTG	CAG	ATC	CAA	AGT	ACC	ACA	GCA	AAA	GAA	744
	Tyr	Lys	Gly	Arg	Ile	Thr	Leu	Gln	Ile	Gln	Ser	Thr	Thr	Ala	Lys	Glu	
				195					200					205			
15	TTC	ACA	GTC	ACC	ATC	AAG	CAT	TTG	CAG	CTC	AAT	GAT	GCT	GGG	CAG	TAT	792
	Phe	Thr	Val	Thr	Ile	Lys	His	Leu	Gln	Leu	Asn	Asp	Ala	Gly	Gln	Tyr	
			210					215					220				
20	GTC	TGC	CAG	AGT	GGA	AGC	GAC	CCC	ACT	GCT	GAA	GAA	CAG	AAC	GTT	GAC	840
	Val	Cys	Gln	Ser	Gly	Ser	Asp	Pro	Thr	Ala	Glu	Glu	Gln	Asn	Val	Asp	
		225					230					235					
25	CTC	CGA	CTG	CTA	ACT	CCT	GGT	CTG	CTC	TAT	GGA	AAC	CTG	GGG	GGC	TCG	888
	Leu	Arg	Leu	Leu	Thr	Pro	Gly	Leu	Leu	Tyr	Gly	Asn	Leu	Gly	Gly	Ser	
	240					245					250					255	
30	GTG	ACC	TTT	GAA	TGT	GCC	CTG	GAC	TCT	GAA	GAC	GCA	AAC	GCG	GTA	GCA	936
	Val	Thr	Phe	Glu	Cys	Ala	Leu	Asp	Ser	Glu	Asp	Ala	Asn	Ala	Val	Ala	
					260					265					270		
35	TCC	TTG	CGC	CAG	GTT	AGG	GGT	GGC	AAT	GTG	GTC	ATT	GAC	AGC	CAG	GGG	984
	Ser	Leu	Arg	Gln	Val	Arg	Gly	Gly	Asn	Val	Val	Ile	Asp	Ser	Gln	Gly	
				275					280					285			
40	ACA	ATA	GAT	CCA	GCC	TTC	GAG	GGC	AGG	ATC	CTG	TTC	ACC	AAG	GCT	GAG	1032
	Thr	Ile	Asp	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Phe	Thr	Lys	Ala	Glu	
			290					295					300				
45	AAC	GGC	CAC	TTC	AGT	GTA	GTG	ATC	GCA	GGC	CTG	AGG	AAG	GAA	GAC	ACA	1080
	Asn	Gly	His	Phe	Ser	Val	Val	Ile	Ala	Gly	Leu	Arg	Lys	Glu	Asp	Thr	
		305					310					315					
50	GGG	AAC	TAT	CTG	TGC	GGA	GTC	CAG	TCC	AAT	GGT	CAG	TCT	GGG	GAT	GGG	1128
	Gly	Asn	Tyr	Leu	Cys	Gly	Val	Gln	Ser	Asn	Gly	Gln	Ser	Gly	Asp	Gly	
	320					325					330					335	
55	CCC	ACC	CAG	CTT	CGG	CAA	CTC	TTC	GTC	AAT	GAA	GAG	ATC	GAC	GTG	TCC	1176
	Pro	Thr	Gln	Leu	Arg	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ile	Asp	Val	Ser	
					340					345					350		
60	CGC	AGC	CCC	CCT	GTG	TTG	AAG	GGC	TTT	CCA	GGA	GGC	TCC	GTG	ACC	ATA	1224
	Arg	Ser	Pro	Pro	Val	Leu	Lys	Gly	Phe	Pro	Gly	Gly	Ser	Val	Thr	Ile	
				355					360					365			
65	CGC	TGC	CCC	TAC	AAC	CCG	AAG	AGA	AGC	GAC	AGC	CAC	CTG	CAG	CTG	TAT	1272
	Arg	Cys	Pro	Tyr	Asn	Pro	Lys	Arg	Ser	Asp	Ser	His	Leu	Gln	Leu	Tyr	
			370					375					380				
70	CTC	TGG	GAA	GGG	AGT	CAA	ACC	CGC	CAT	CTG	CTG	GTG	GAC	AGC	GGC	GAG	1320
	Leu	Trp	Glu	Gly	Ser	Gln	Thr	Arg	His	Leu	Leu	Val	Asp	Ser	Gly	Glu	
		385					390					395					
75	GGG	CTG	GTT	CAG	AAA	GAC	TAC	ACA	GGC	AGG	CTG	GCC	CTG	TTC	GAA	GAG	1368
	Gly	Leu	Val	Gln	Lys	Asp	Tyr	Thr	Gly	Arg	Leu	Ala	Leu	Phe	Glu	Glu	
	400					405					410					415	
80	CCT	GGC	AAT	GGC	ACC	TTC	TCA	GTC	GTC	CTC	AAC	CAG	CTC	ACT	GCC	GAG	1416
	Pro	Gly	Asn	Gly	Thr	Phe	Ser	Val	Val	Leu	Asn	Gln	Leu	Thr	Ala	Glu	
					420					425					430		

	GAT Asp	GAA Glu	GGC Gly	TTC Phe	TAC Tyr	TGG Trp	TGT Cys	GTC Val	AGC Ser	GAT Asp	GAC Asp	GAT Asp	GAG Glu	TCC Ser	CTG Leu	ACG Thr	1464
				435					440					445			
5	ACT Thr	TCG Ser	GTG Val	AAG Lys	CTC Leu	CAG Gln	ATC Ile	GTT Val	GAC Asp	GGA Gly	GAA Glu	CCA Pro	AGC Ser	CCC Pro	ACG Thr	ATC Ile	1512
			450					455					460				
10	GAC Asp	AAG Lys	TTC Phe	ACT Thr	GCT Ala	GTG Val	CAG Gln	GGA Gly	GAG Glu	CCT Pro	GTT Val	GAG Glu	ATC Ile	ACC Thr	TGC Cys	CAC His	1560
			465				470						475				
15	TTC Phe	CCA Pro	TGC Cys	AAA Lys	TAC Tyr	TTC Phe	TCC Ser	TCC Ser	GAG Glu	AAG Lys	TAC Tyr	TGG Trp	TGC Cys	AAG Lys	TGG Trp	AAT Asn	1608
	480					485					490					495	
20	GAC Asp	CAT His	GGC Gly	TGC Cys	GAG Glu	GAC Asp	CTG Leu	CCC Pro	ACT Thr	AAG Lys	CTC Leu	AGC Ser	TCC Ser	AGC Ser	GGC Gly	GAC Asp	1656
					500					505					510		
25	CTT Leu	GTG Val	AAA Lys	TGC Cys	AAC Asn	AAC Asn	AAC Asn	CTG Leu	GTC Val	CTC Leu	ACC Thr	CTG Leu	ACC Thr	TTG Leu	GAC Asp	TCG Ser	1704
				515				520						525			
30	GTC Val	AGC Ser	GAA Glu	GAT Asp	GAC Asp	GAG Glu	GGC Gly	TGG Trp	TAC Tyr	TGG Trp	TGT Cys	GGC Gly	GCG Ala	AAA Lys	GAC Asp	GGG Gly	1752
			530					535					540				
35	CAC His	GAG Glu	TTT Phe	GAA Glu	GAG Glu	GTT Val	GCG Ala	GCC Ala	GTC Val	AGG Arg	GTG Val	GAG Glu	CTG Leu	ACA Thr	GAG Glu	CCA Pro	1800
			545				550					555					
40	GCC Ala	AAG Lys	GTA Val	GCT Ala	GTC Val	GAG Glu	CCA Pro	GCC Ala	AAG Lys	GTA Val	CCT Pro	GTC Val	GAC Asp	CCA Pro	GCC Ala	AAG Lys	1848
	560					565					570					575	
45	GCA Ala	GCC Ala	CCC Pro	GCG Ala	CCT Pro	GCT Ala	GAG Glu	GAG Glu	AAG Lys	GCC Ala	AAG Lys	GCG Ala	CGG Arg	TGC Cys	CCA Pro	GTG Val	1896
					580					585					590		
50	CCC Pro	AGG Arg	AGA Arg	AGG Arg	CAG Gln	TGG Trp	TAC Tyr	CCA Pro	TTG Leu	TCA Ser	AGG Arg	AAG Lys	CTG Leu	AGA Arg	ACA Thr	AGT Ser	1944
					595				600					605			
55	TGT Cys	CCA Pro	GAA Glu	CCT Pro	CGG Arg	CTC Leu	CTT Leu	GCG Ala	GAG Glu	GAG Glu	GTA Val	GCA Ala	GTG Val	CAG Gln	AGT Ser	GCG Ala	1992
			610					615					620				
60	GAA Glu	GAC Asp	CCA Pro	GCC Ala	AGT Ser	GGG Gly	AGC Ser	AGA Arg	GCG Ala	TCT Ser	GTG Val	GAT Asp	GCC Ala	AGC Ser	AGT Ser	GCT Ala	2040
			625				630					635					
65	TCG Ser	GGA Gly	CAA Gln	AGC Ser	GGG Gly	AGT Ser	GCC Ala	AAA Lys	GTA Val	CTG Leu	ATC Ile	TCC Ser	ACC Thr	CTG Leu	GTG Val	CCC Pro	2088
					645						650					655	
70	TTG Leu	GGG Gly	CTG Leu	GTG Val	CTG Ala	GCA Ala	GCG Ala	GGG Gly	GCC Ala	ATG Met	GCC Ala	GTG Val	GCC Ala	ATA Ile	GCC Ala	AGA Arg	2136
					660					665					670		
75	GCC Ala	CGG Arg	CAC His	AGG Arg	AGG Arg	AAC Asn	GTG Val	GAC Asp	CGA Arg	GTT Val	TCC Ser	ATC Ile	GGA Gly	AGC Ser	TAC Tyr	AGG Arg	2184
				675					680					685			
80	ACA Thr	GAC Asp	ATT Ile	AGC Ser	ATG Met	TCA Ser	GAC Asp	TTG Leu	GAG Glu	AAC Asn	TCC Ser	AGG Arg	GAG Glu	TTC Phe	GGA Gly	GCC Ala	2232

	690	695	700	
5	ATT GAC AAC CCA AGC GCC TGC CCC GAT GCC CGG GAG ACG GGC CTC GGA Ile Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly 705 710 715	2280		
10	GGA AAG GAT GAG TTA GCG ACG GCC ACC GAG AGC ACC GTG GAG ATT GAG Gly Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu 720 725 730 735	2328		
15	GAG CCC AAG AAG GCA AAA CGG TCA TCC AAG GAA GAA GCC GAC CTG GCC Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala 740 745 750	2376		
20	TAC TCA GCT TTC CTG CTC CAA TCC AAC ACC ATA GCT GCT GAG CAC CAA Tyr Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln 755 760 765	2424		
25	GAT GGC CCC AAG GAG GCC TAG GCACAGCCGG CCACCGCCGC CGCCGCCACC GCCGC Asp Gly Pro Lys Glu Ala 770	2480		
30	CGCCGCCGCC ACCTGTGAAA ATCACCTTCC AGAATCACGT TGATCCTCGG GTCCCCAGA GCCGGGGGCT CAACCGCCCT GCACCCCCCA TGTCCCCACC ACCTAAACTT CCCTACCTGT GCCAGAGGT GTGCTGGTCC CCTCCTCCAC GGCATCCAGG CCTGGCTCAA TGTTCCTGTT GGGGTGGGGG TGTGAGGGGT TCCTACTTGC AGCCCGGTTT TCCCGAGAGA AGCTAAGGAT CCAGGTCTCTG AGGGAGGGGC CTCTCGAAGG CAGACAGACC AGAGAGGGGG GAGGAGCCCT TGGATGGGAG GCCAGAGGCG CTTTCCGGCC ACCCCTCCC TCCCTGCCCC CACCCTCCTT CCTTCATTCA AAAGTCCCAG TGGCTGCTGC CTAGGTCCA GCGCTGGCC GCACGCCTCC TCGAAGCCGT TGTGCAAACA TCACTGGAGG AAGCCAGGGC TCCTCCCGGG CTGTGTATCC TCACTCAGGC ATCCTGTCCT CCCCAGTATC AGGAGATGTC AAGCGTCTGA AGGCTGTGTG CCCTGGGCGT GTCTGCAAGT CACCCAGAC ACATGTTCTC GCCATTTTAC AGATGAGAAC ACTGAGGTTG TACTCAAGGG CACCCTGCGA GATGGAGCAA CAGCAAACTA GATGGGCTTC TGCTGTCCTC TTGGCCAGAG GTCTCTCCAC AGGAGCCCCT GCCCCTGTAG GAAGCAGAGT TTTAGAACAT GGAAGAAGAA GAGGGGGATG GCCCTGGACG CTGACCTCTC CCAAGCCCCC ACGGGGGAAA AGGCCCCCTC CTTTTCTGTC ACTCTCGGGG ACCTGCGGAG TTGAGCATTC GTGCCCCGTG TGTCTGAAGA GTTCCCAGTG GAAAGAAGAA AAGAGGGTGT TTGTCAGTGC CGGGGAGGGC CTGATCCCCA GACAGCTGAA GTTTAAGGTC CTTGTCCCTG TGAGCTTTAA CCAGCACCTC CGGGCTGACC CTTGCTAACA CATCAGAAAT GTGATTTAAT CATTAAACAT TGTGATTGCC ACTGGGA	2540 2600 2660 2720 2780 2840 2900 2960 3020 3080 3140 3200 3260 3320 3380 3440 3500 3517		

60

(2) INFORMATION FOR SEQ ID NO: 2:

65 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 amino acids

5

	Met	Ala	Leu	Phe	Leu	Thr	Cys	Leu	Leu	Ala	Val	Phe	Ser	Ala	Ala
10	1				5			10						15	
	Thr	Ala	Gln	Ser	Ser	Leu	Leu	Gly	Pro	Ser	Ser	Ile	Phe	Gly	Pro Gly
			20					25						30	
15	Glu	Val	Asn	Val	Leu	Glu	Gly	Asp	Ser	Val	Ser	Ile	Thr	Cys	Tyr Tyr
			35					40					45		
	Pro	Thr	Thr	Ser	Val	Thr	Arg	His	Ser	Arg	Lys	Phe	Trp	Cys	Arg Glu
							55					60			
20	Glu	Glu	Ser	Gly	Arg	Cys	Val	Thr	Leu	Ala	Ser	Thr	Gly	Tyr	Thr Ser
	65					70					75				80
	Gln	Glu	Tyr	Ser	Gly	Arg	Gly	Lys	Leu	Thr	Asp	Phe	Pro	Asp	Lys Gly
					85					90					95
25	Glu	Phe	Val	Val	Thr	Val	Asp	Gln	Leu	Thr	Gln	Asn	Asp	Ser	Gly Ser
				100					105					110	
30	Tyr	Lys	Cys	Gly	Val	Gly	Val	Asn	Gly	Arg	Gly	Leu	Asp	Phe	Gly Val
			115					120					125		
	Asn	Val	Leu	Val	Ser	Gln	Lys	Pro	Glu	Pro	Asp	Asp	Val	Val	Tyr Lys
			130					135				140			
35	Gln	Tyr	Glu	Ser	Tyr	Thr	Val	Thr	Ile	Thr	Cys	Pro	Phe	Thr	Tyr Ala
	145					150					155				160
	Thr	Arg	Gln	Leu	Lys	Lys	Ser	Phe	Tyr	Lys	Val	Glu	Asp	Gly	Glu Leu
					165					170					175
40	Val	Leu	Ile	Ile	Asp	Ser	Ser	Ser	Lys	Glu	Ala	Lys	Asp	Pro	Arg Tyr
				180					185					190	
	Lys	Gly	Arg	Ile	Thr	Leu	Gln	Ile	Gln	Ser	Thr	Thr	Ala	Lys	Glu Phe
			195					200					205		
45	Thr	Val	Thr	Ile	Lys	His	Leu	Gln	Leu	Asn	Asp	Ala	Gly	Gln	Tyr Val
			210				215					220			
50	Cys	Gln	Ser	Gly	Ser	Asp	Pro	Thr	Ala	Glu	Glu	Gln	Asn	Val	Asp Leu
	225					230					235				240
	Arg	Leu	Leu	Thr	Pro	Gly	Leu	Leu	Tyr	Gly	Asn	Leu	Gly	Gly	Ser Val
					245					250					255
55	Thr	Phe	Glu	Cys	Ala	Leu	Asp	Ser	Glu	Asp	Ala	Asn	Ala	Val	Ala Ser
				260					265					270	
	Leu	Arg	Gln	Val	Arg	Gly	Gly	Asn	Val	Val	Ile	Asp	Ser	Gln	Gly Thr
			275					280					285		
60	Ile	Asp	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Phe	Thr	Lys	Ala	Glu Asn
		290					295					300			
65	Gly	His	Phe	Ser	Val	Val	Ile	Ala	Gly	Leu	Arg	Lys	Glu	Asp	Thr Gly
	305					310					315				320

	Asn	Tyr	Leu	Cys	Gly	Val	Gln	Ser	Asn	Gly	Gln	Ser	Gly	Asp	Gly	Pro
					325					330					335	
5	Thr	Gln	Leu	Arg	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ile	Asp	Val	Ser	Arg
				340					345					350		
	Ser	Pro	Pro	Val	Leu	Lys	Gly	Phe	Pro	Gly	Gly	Ser	Val	Thr	Ile	Arg
				355				360					365			
10	Cys	Pro	Tyr	Asn	Pro	Lys	Arg	Ser	Asp	Ser	His	Leu	Gln	Leu	Tyr	Leu
				370			375					380				
	Trp	Glu	Gly	Ser	Gln	Thr	Arg	His	Leu	Leu	Val	Asp	Ser	Gly	Glu	Gly
	385					390					395					400
15	Leu	Val	Gln	Lys	Asp	Tyr	Thr	Gly	Arg	Leu	Ala	Leu	Phe	Glu	Glu	Pro
					405					410					415	
	Gly	Asn	Gly	Thr	Phe	Ser	Val	Val	Leu	Asn	Gln	Leu	Thr	Ala	Glu	Asp
				420					425					430		
	Glu	Gly	Phe	Tyr	Trp	Cys	Val	Ser	Asp	Asp	Asp	Glu	Ser	Leu	Thr	Thr
			435					440					445			
25	Ser	Val	Lys	Leu	Gln	Ile	Val	Asp	Gly	Glu	Pro	Ser	Pro	Thr	Ile	Asp
				450			455					460				
	Lys	Phe	Thr	Ala	Val	Gln	Gly	Glu	Pro	Val	Glu	Ile	Thr	Cys	His	Phe
	465					470					475					480
30	Pro	Cys	Lys	Tyr	Phe	Ser	Ser	Glu	Lys	Tyr	Trp	Cys	Lys	Trp	Asn	Asp
					485					490					495	
	His	Gly	Cys	Glu	Asp	Leu	Pro	Thr	Lys	Leu	Ser	Ser	Ser	Gly	Asp	Leu
				500					505					510		
	Val	Lys	Cys	Asn	Asn	Asn	Leu	Val	Leu	Thr	Leu	Thr	Leu	Asp	Ser	Val
			515					520					525			
40	Ser	Glu	Asp	Asp	Glu	Gly	Trp	Tyr	Trp	Cys	Gly	Ala	Lys	Asp	Gly	His
		530					535					540				
	Glu	Phe	Glu	Glu	Val	Ala	Ala	Val	Arg	Val	Glu	Leu	Thr	Glu	Pro	Ala
	545					550					555					560
45	Lys	Val	Ala	Val	Glu	Pro	Ala	Lys	Val	Pro	Val	Asp	Pro	Ala	Lys	Ala
					565					570					575	
	Ala	Pro	Ala	Pro	Ala	Glu	Glu	Lys	Ala	Lys	Ala	Arg	Cys	Pro	Val	Pro
				580					585					590		
50	Arg	Arg	Arg	Gln	Trp	Tyr	Pro	Leu	Ser	Arg	Lys	Leu	Arg	Thr	Ser	Cys
			595					600					605			
55	Pro	Glu	Pro	Arg	Leu	Leu	Ala	Glu	Glu	Val	Ala	Val	Gln	Ser	Ala	Glu
		610					615					620				
	Asp	Pro	Ala	Ser	Gly	Ser	Arg	Ala	Ser	Val	Asp	Ala	Ser	Ser	Ala	Ser
	625					630					635					640
60	Gly	Gln	Ser	Gly	Ser	Ala	Lys	Val	Leu	Ile	Ser	Thr	Leu	Val	Pro	Leu

25 (2) INFORMATION FOR SEQ ID NO: 3:

```

30      (A)   LENGTH:           2919 base pairs
      (B)   TYPE:             nucleic acid
      (C)   STRANDEDNESS:     single
      (D)   TOPOLOGY:         linear
      DESCRIPTION:             Human polyimmunoglobulin Receptor

```

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 235....2472

	AGAGTTTCAG	TTTTGGCAGC	AGCGTCCAGT	GCCCTGCCAG	TAGCTCCTAG	AGAGGCAGGG		60
45	GTTACCAACT	GGCCAGCAGG	CTGTGTCCCT	GAAGTCAGAT	CAACGGGAGA	GAAGGAAGTG		120
	GCTAAACAT	TGCACAGGAG	AAGTCGGCCT	GAGTGGTGCG	GCGCTCGGGA	CCCACCAGCA		180
50	ATGCTGCTCT	TCGTGCTCAC	CTGCCTGCTG	GCGGTCTTCC	CAGCCATCTC	CACG AAG		237
						Lys 1		
	AGT CCC ATA	TTT GGT CCC	GAG GAG GTG	AAT AGT GTG	GAA GGT AAC	TCA		285
	Ser Pro Ile	Phe Gly Pro	Glu Glu Val	Asn Ser Val	Glu Gly Asn	Ser		
		5		10	15			
55	GTG TCC ATC	ACG TGC TAC	TAC CCA CCC	ACC TCT GTC	AAC CGG CAC	ACC		333
	Val Ser Ile	Thr Cys Tyr	Tyr Pro Pro	Thr Ser Val	Asn Arg His	Thr		
		20	25		30			
60	CGG AAG TAC	TGG TGC CGG	CAG GGA GCT	AGA GGT GGC	TGC ATA ACC	CTC		381
	Arg Lys Tyr	Trp Cys Arg	Gln Gly Ala	Arg Gly Gly	Cys Ile Thr	Leu		
		35	40	45				
65	ATC TCC TCG	GAG GGC TAC	GTC TCC AGC	AAA TAT GCA	GGC AGG GCT	AAC		429
	Ile Ser Ser	Glu Gly Tyr	Val Ser Ser	Lys Tyr Ala	Gly Arg Ala	Asn		
	50	55	60	65				

	CTC	ACC	AAC	TTC	CCG	GAG	AAC	GGC	ACA	TTT	GTG	AAC	ATT	GCC	CAG		477
	Leu	Thr	Asn	Phe	Pro	Glu	Asn	Gly	Thr	Phe	Val	Val	Asn	Ile	Ala	Gln	
					70					75					80		
5	CTG	AGC	CAG	GAT	GAC	TCC	GGG	CGC	TAC	AAG	TGT	GGC	CTG	GGC	ATC	AAT	525
	Leu	Ser	Gln	Asp	Asp	Ser	Gly	Arg	Tyr	Lys	Cys	Gly	Leu	Gly	Ile	Asn	
				85					90					95			
10	AGC	CGA	GGC	CTG	TCC	TTT	GAT	GTC	AGC	CTG	GAG	GTC	AGC	CAG	GGT	CCT	573
	Ser	Arg	Gly	Leu	Ser	Phe	Asp	Val	Ser	Leu	Glu	Val	Ser	Gln	Gly	Pro	
			100					105					110				
15	GGG	CTC	CTA	AAT	GAC	ACT	AAA	GTC	TAC	ACA	GTG	GAC	CTG	GGC	AGA	ACG	621
	Gly	Leu	Leu	Asn	Asp	Thr	Lys	Val	Tyr	Thr	Val	Asp	Leu	Gly	Arg	Thr	
			115				120					125					
20	GTG	ACC	ATC	AAC	TGC	CCT	TTC	AAG	ACT	GAG	AAT	GCT	CAA	AAG	AGG	AAG	669
	Val	Thr	Ile	Asn	Cys	Pro	Phe	Lys	Thr	Glu	Asn	Ala	Gln	Lys	Arg	Lys	
	130					135					140					145	
25	TCC	TTG	TAC	AAG	CAG	ATA	GGC	CTG	TAC	CCT	GTG	CTG	GTC	ATC	GAC	TCC	717
	Ser	Leu	Tyr	Lys	Gln	Ile	Gly	Leu	Tyr	Pro	Val	Leu	Val	Ile	Asp	Ser	
				150						155					160		
30	AGT	GGT	TAT	GTG	AAT	CCC	AAC	TAT	ACA	GGA	AGA	ATA	CGC	CTT	GAT	ATT	765
	Ser	Gly	Tyr	Val	Asn	Pro	Asn	Tyr	Thr	Gly	Arg	Ile	Arg	Leu	Asp	Ile	
				165				170						175			
35	CAG	GGT	ACT	GGC	CAG	TTA	CTG	TTC	AGC	GTT	GTC	ATC	AAC	CAA	CTC	AGG	813
	Gln	Gly	Thr	Gly	Gln	Leu	Leu	Phe	Ser	Val	Val	Ile	Asn	Gln	Leu	Arg	
			180					185					190				
40	CTC	AGC	GAT	GCT	GGG	CAG	TAT	CTC	TGC	CAG	GCT	GGG	GAT	GAT	TCC	AAT	861
	Leu	Ser	Asp	Ala	Gly	Gln	Tyr	Leu	Cys	Gln	Ala	Gly	Asp	Asp	Ser	Asn	
			195				200					205					
45	AGT	AAT	AAG	AAG	AAT	GCT	GAC	CTC	CAA	GTG	CTA	AAG	CCC	GAG	CCC	GAG	909
	Ser	Asn	Lys	Lys	Asn	Ala	Asp	Leu	Gln	Val	Leu	Lys	Pro	Glu	Pro	Glu	
	210				215					220						225	
50	CTG	GTT	TAT	GAA	GAC	CTG	AGG	GGC	TCA	GTG	ACC	TTC	CAC	TGT	GCC	CTG	957
	Leu	Val	Tyr	Glu	Asp	Leu	Arg	Gly	Ser	Val	Thr	Phe	His	Cys	Ala	Leu	
				230					235						240		
55	GGC	CCT	GAG	GTG	GCA	AAC	GTG	GCC	AAA	TTT	CTG	TGC	CGA	CAG	AGC	AGT	1005
	Gly	Pro	Glu	Val	Ala	Asn	Val	Ala	Lys	Phe	Leu	Cys	Arg	Gln	Ser	Ser	
				245				250						255			
60	GGG	GAA	AAC	TGT	GAC	GTG	GTC	GTC	AAC	ACC	CTG	GGG	AAG	AGG	GCC	CCA	1053
	Gly	Glu	Asn	Cys	Asp	Val	Val	Val	Asn	Thr	Leu	Gly	Lys	Arg	Ala	Pro	
			260				265						270				
65	GCC	TTT	GAG	GGC	AGG	ATC	CTG	CTC	AAC	CCC	CAG	GAC	AAG	GAT	GGC	TCA	1101
	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Leu	Asn	Pro	Gln	Asp	Lys	Asp	Gly	Ser	
		275				280						285					
70	TTC	AGT	GTG	GTG	ATC	ACA	GGC	CTG	AGG	AAG	GAG	GAT	GCA	GGG	CGC	TAC	1149
	Phe	Ser	Val	Val	Ile	Thr	Gly	Leu	Arg	Lys	Glu	Asp	Ala	Gly	Arg	Tyr	
		290				295					300					305	
75	CTG	TGT	GGA	GCC	CAT	TCG	GAT	GGT	CAG	CTG	CAG	GAA	GGC	TCG	CCT	ATC	1197
	Leu	Cys	Gly	Ala	His	Ser	Asp	Gly	Gln	Leu	Gln	Glu	Gly	Ser	Pro	Ile	
				310						315					320		
80	CAG	GCC	TGG	CAA	CTC	TTC	GTC	AAT	GAG	GAG	TCC	ACG	ATT	CCC	CGC	AGC	1245
	Gln	Ala	Trp	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ser	Thr	Ile	Pro	Arg	Ser	

	325	330	335	
5	CCC ACT GTG GTG AAG GGG GTG GCA GGA AGC TCT GTG GCC GTG CTC TGC Pro Thr Val Val Lys Gly Val Ala Gly Ser Ser Val Ala Val Leu Cys 340 345 350			1293
10	CCC TAC AAC CGT AAG GAA AGC AAA AGC ATC AAG TAC TGG TGT CTC TGG Pro Tyr Asn Arg Lys Glu Ser Lys Ser Ile Lys Tyr Trp Cys Leu Trp 355 360 365			1341
15	GAA GGG GCC CAG AAT GGC CGC TGC CCC CTG CTG GTG GAC AGC GAG GGG Glu Gly Ala Gln Asn Gly Arg Cys Pro Leu Leu Val Asp Ser Glu Gly 370 375 380 385			1389
20	TGG GTT AAG GCC CAG TAC GAG GGC CGC CTC TCC CTG CTG GAG GAG CCA Trp Val Lys Ala Gln Tyr Glu Gly Arg Leu Ser Leu Leu Glu Glu Pro 390 395 400			1437
25	GGC AAC GGC ACC TTC ACT GTC ATC CTC AAC CAG CTC ACC AGC CGG GAC Gly Asn Gly Thr Phe Thr Val Ile Leu Asn Gln Leu Thr Ser Arg Asp 405 410 415			1485
30	GCC GGC TTC TAC TGG TGT CTG ACC AAC GGC GAT ACT CTC TGG AGG ACC Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Thr Leu Trp Arg Thr 420 425 430			1533
35	ACC GTG GAG ATC AAG ATT ATC GAA GGA GAA CCA AAC CTC AAG GTA CCA Thr Val Glu Ile Lys Ile Ile Glu Gly Glu Pro Asn Leu Lys Val Pro 435 440 445			1581
40	GGG AAT GTC ACG GCT GTG CTG GGA GAG ACT CTC AAG GTC CCC TGT CAC Gly Asn Val Thr Ala Val Leu Gly Glu Thr Leu Lys Val Pro Cys His 450 455 460 465			1629
45	TTT CCA TGC AAA TTC TCC TCG TAC GAG AAA TAC TGG TGC AAG TGG AAT Phe Pro Cys Lys Phe Ser Ser Tyr Glu Lys Tyr Trp Cys Lys Trp Asn 470 475 480			1677
50	AAC ACG GGC TGC CAG GCC CTG CCC AGC CAA GAC GAA GGC CCC AGC AAG Asn Thr Gly Cys Gln Ala Leu Pro Ser Gln Asp Glu Gly Pro Ser Lys 485 490 495			1725
55	GCC TTC GTG AAC TGT GAC GAG AAC AGC CGG CTT GTC TCC CTG ACC CTG Ala Phe Val Asn Cys Asp Glu Asn Ser Arg Leu Val Ser Leu Thr Leu 500 505 510			1773
60	AAC CTG GTG ACC AGG GCT GAT GAG GGC TGG TAC TGG TGT GGA GTG AAG Asn Leu Val Thr Arg Ala Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys 515 520 525			1821
65	CAG GGC CAC TTC TAT GGA GAG ACT GCA GCC GTC TAT GTG GCA GTT GAA Gln Gly His Phe Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu 530 535 540 545			1869
70	GAG AGG AAG GCA GCG GGG TCC CGC GAT GTC AGC CTA GCG AAG GCA GAC Glu Arg Lys Ala Ala Gly Ser Arg Asp Val Ser Leu Ala Lys Ala Asp 550 555 560			1917
75	GCT GCT CCT GAT GAG AAG GTG CTA GAC TCT GGT TTT CGG GAG ATT GAG Ala Ala Pro Asp Glu Lys Val Leu Asp Ser Gly Phe Arg Glu Ile Glu 565 570 575			1965
80	AAC AAA GCC ATT CAG GAT CCC AGG CTT TTT GCA GAG GAA AAG GCG GTG Asn Lys Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala Val 580 585 590			2013

1293
 1341
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 1869
 1917
 1965
 2013

GCA GAT ACA AGA GAT CAA GCC GAT GGG AGC AGA GCA TCT GTG GAT TCC 2061
 Ala Asp Thr Arg Asp Gln Ala Asp Gly Ser Arg Ala Ser Val Asp Ser
 595 600 605
 5 GGC AGC TCT GAG GAA CAA GGT GGA AGC TCC AGA GCG CTG GTC TCC ACC 2109
 Gly Ser Ser Glu Glu Gln Gly Gly Ser Ser Arg Ala Leu Val Ser Thr
 610 615 620 625
 10 CTG GTG CCC CTG GGC CTG GTG CTG GCA GTG GGA GCC GTG GCT GTG GGG 2157
 Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Gly
 630 635 640
 15 GTG GCC AGA GCC CGG CAC AGG AAG AAC GTC GAC CGA GTT TCA ATC AGA 2205
 Val Ala Arg Ala Arg His Arg Lys Asn Val Asp Arg Val Ser Ile Arg
 645 650 655
 AGC TAC AGG ACA GAC ATT AGC ATG TCA GAC TTC GAG AAC TCC AGG GAA 2253
 Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Glu
 660 665 670
 20 TTT GGA GCC AAT GAC AAC ATG GGA GCC TCT TCG ATC ACT CAG GAG ACA 2301
 Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu Thr
 675 680 685
 25 TCC CTC GGA GGA AAA GAA GAG TTT GTT GCC ACC ACT GAG AGC ACC ACA 2349
 Ser Leu Gly Gly Lys Glu Glu Phe Val Ala Thr Thr Glu Ser Thr Thr
 690 695 700 705
 30 GAG ACC AAA GAA CCC AAG AAG GCA AAA AGG TCA TCC AAG GAG GAA GCC 2397
 Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala
 710 715 720
 35 GAG ATG GCC TAC AAA GAC TTC CTG CTC CAG TCC AGC ACC GTG GCC GCC 2445
 Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala Ala
 725 730 735
 GAG GCC CAG GAC GGC CCC CAG GAA GCC TAGACGGTGT CGCCGCCTGC TCCCTGCA 2500
 Glu Ala Gln Asp Gly Pro Gln Glu Ala
 740 745
 40 CCCATGACAA TCACCTTCAG AATCATGTCG ATCCTGGGGG CCCTCAGCTC CTGGGGACCC 2560
 CACTCCCTGC TCTAACACCT GCCTAGGTTT TTCCTACTGT CCTCAGAGGC GTGCTGGTCC 2620
 45 CCTCCTCAGT GACATCAAAG CCTGGCCTAA TTGTTCTTAT TGGGGATGAG GGTGGCATGA 2680
 GGAGGTCCCA CTTGCAACTT CTTTCTGTTG AGAGAACCTC AGGTACGGAG AAGAATAGAG 2740
 GTCCTCATGG GTCCCTTGAA GGAAGAGGGA CCAGGGTGGG AGAGCTGATT GCAGAAAGGA 2800
 50 GAGACGTGCA GCGCCCCTCT GCACCCTTAT CATGGGATGT CAACAGAATT TTTTCCCTCC 2860
 ACTCCATCCC TCCCTCCCGT CCTTCCCCTC TTCTTCTTTC CTTACCATCA AAAGATGTA 2919

55

(2) INFORMATION FOR SEQ ID NO: 4:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 746 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear
 65 DESCRIPTION: Human Polyimmunoglobulin Receptor

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

5	Lys 1	Ser	Pro	Ile 5	Phe	Gly	Pro	Glu	Glu	Val 10	Asn	Ser	Val	Glu	Gly	Asn 15
	Ser	Val	Ser	Ile 20	Thr	Cys	Tyr	Tyr	Pro 25	Pro	Thr	Ser	Val	Asn 30	Arg	His
10	Thr	Arg	Lys 35	Tyr	Trp	Cys	Arg	Gln 40	Gly	Ala	Arg	Gly	Gly 45	Cys	Ile	Thr
	Leu	Ile	Ser	Ser	Glu	Gly	Tyr 55	Val	Ser	Ser	Lys	Tyr 60	Ala	Gly	Arg	Ala
15	Asn 65	Leu	Thr	Asn	Phe	Pro 70	Glu	Asn	Gly	Thr	Phe 75	Val	Val	Asn	Ile	Ala 80
	Gln	Leu	Ser	Gln	Asp 85	Asp	Ser	Gly	Arg	Tyr 90	Lys	Cys	Gly	Leu	Gly 95	Ile
20	Asn	Ser	Arg	Gly 100	Leu	Ser	Phe	Asp	Val 105	Ser	Leu	Glu	Val	Ser 110	Gln	Gly
	Pro	Gly	Leu 115	Leu	Asn	Asp	Thr	Lys 120	Val	Tyr	Thr	Val	Asp 125	Leu	Gly	Arg
25	Thr	Val 130	Thr	Ile	Asn	Cys	Pro 135	Phe	Lys	Thr	Glu	Asn 140	Ala	Gln	Lys	Arg
30	Lys 145	Ser	Leu	Tyr	Lys	Gln 150	Ile	Gly	Leu	Tyr	Pro 155	Val	Leu	Val	Ile	Asp 160
	Ser	Ser	Gly	Tyr	Val 165	Asn	Pro	Asn	Tyr	Thr 170	Gly	Arg	Ile	Arg	Leu 175	Asp
35	Ile	Gln	Gly	Thr 180	Gly	Gln	Leu	Leu	Phe 185	Ser	Val	Val	Ile	Asn 190	Gln	Leu
	Arg	Leu 195	Ser	Asp	Ala	Gly	Gln	Tyr 200	Leu	Cys	Gln	Ala	Gly 205	Asp	Asp	Ser
40	Asn 210	Ser	Asn	Lys	Lys	Asn 215	Ala	Asp	Leu	Gln	Val	Leu 220	Lys	Pro	Glu	Pro
45	Glu 225	Leu	Val	Tyr	Glu	Asp 230	Leu	Arg	Gly	Ser	Val 235	Thr	Phe	His	Cys	Ala 240
	Leu	Gly	Pro	Glu	Val 245	Ala	Asn	Val	Ala	Lys 250	Phe	Leu	Cys	Arg	Gln	Ser 255
50	Ser	Gly	Glu	Asn 260	Cys	Asp	Val	Val	Val 265	Asn	Thr	Leu	Gly	Lys 270	Arg	Ala
	Pro	Ala	Phe 275	Glu	Gly	Arg	Ile	Leu 280	Leu	Asn	Pro	Gln	Asp 285	Lys	Asp	Gly
55	Ser	Phe 290	Ser	Val	Val	Ile	Thr 295	Gly	Leu	Arg	Lys	Glu 300	Asp	Ala	Gly	Arg
60	Tyr 305	Leu	Cys	Gly	Ala	His 310	Ser	Asp	Gly	Gln	Leu 315	Gln	Glu	Gly	Ser	Pro 320
	Ile	Gln	Ala	Trp	Gln 325	Leu	Phe	Val	Asn	Glu 330	Glu	Ser	Thr	Ile	Pro 335	Arg
65	Ser	Pro	Thr	Val	Val	Lys	Gly	Val	Ala	Gly	Ser	Ser	Val	Ala	Val	Leu

[illegible]

	690	695	700	
	Thr Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu			
	705	710	715	720
5	Ala Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala			
	725	730	735	
10	Ala Glu Ala Gln Asp Gly Pro Gln Glu Ala			
	740	745		
15	(2) INFORMATION FOR SEQ ID NO: 5:			
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH:	3630 base pairs		
	(B) TYPE:	nucleic acid		
20	(C) STRANDEDNESS:	single		
	(D) TOPOLOGY:	linear		
	DESCRIPTION:	Bovine Polyimmunoglobulin Receptor		
25	(ix) FEATURE:			
	(A) NAME/KEY:	Coding Sequence		
	(B) LOCATION:	152....2425		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:			
	GATCTCCTCG GAGGGTCGTG CAGCGGCCCT GGGTCCCTGC CGGCACCACT ACTTGCGCGT			60
	GTGCTCCCAA AGCTGACGGG ATAGGAGGAA GGAGCTCAA CAACCACACA GGACGGTGGC			120
35	TGGCGGCAGA GACCCGCGGG AGCCCCCAGC G ATG TCG CGC CTG TTC CTC GCC			172
	Met Ser Arg Leu Phe Leu Ala			
	1 5			
40	TGC CTG CTG GCC ATC TTC CCA GTG GTC TCC ATG AAG AGT CCC ATC TTC			220
	Cys Leu Leu Ala Ile Phe Pro Val Val Ser Met Lys Ser Pro Ile Phe			
	10 15 20			
45	GGT CCC GAG GAG GTG AGC AGC GTG GAA GGC CGC TCA GTG TCC ATC AAG			268
	Gly Pro Glu Glu Val Ser Ser Val Glu Gly Arg Ser Val Ser Ile Lys			
	25 30 35			
50	TGC TAC TAC CCG CCC ACC TCC GTC AAC CGG CAC ACG CGC AAG TAC TGG			316
	Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp			
	40 45 50 55			
55	TGC CGG CAG GGA GCC CAG GGC CGC TGC ACG ACC CTC ATC TCC TCG GAG			364
	Cys Arg Gln Gly Ala Gln Gly Arg Cys Thr Thr Leu Ile Ser Ser Glu			
	60 65 70			
55	GGC TAC GTC TCC GAC GAC TAC GTG GGC AGA GCC AAC CTC ACC AAC TTC			412
	Gly Tyr Val Ser Asp Asp Tyr Val Gly Arg Ala Asn Leu Thr Asn Phe			
	75 80 85			
60	CCG GAG AGC GGC ACG TTT GTG GTG GAC ATC AGC CAT CTC ACC CAT AAA			460
	Pro Glu Ser Gly Thr Phe Val Val Asp Ile Ser His Leu Thr His Lys			
	90 95 100			
55	GAC TCA GGG CGC TAC AAG TGT GGC CTG GGC ATT AGC AGC CGT GGC CTT			508
	Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Ser Ser Arg Gly Leu			
	105 110 115			

	AAC	TTC	GAT	GTG	AGC	CTG	GAG	GTC	ATC	AGC	CAA	GAT	CCT	GCA	CAG	GCA	AGT	556
	Asn	Phe	Asp	Val	Ser	Leu	Glu	Val	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Ser		
	120					125					130					135		
5	CAT	GCC	CAC	GTC	TAC	ACT	ATA	GAC	CTG	GGC	AGG	ACT	GTG	ACC	ATC	AAC	604	
	His	Ala	His	Val	Tyr	Thr	Ile	Asp	Leu	Gly	Arg	Thr	Val	Thr	Ile	Asn		
					140					145					150			
10	TGC	CCT	TTC	ACG	CGT	GCG	AAT	TCT	GAG	AAG	AGA	AAA	TCC	TTG	TGC	AAG	652	
	Cys	Pro	Phe	Thr	Arg	Ala	Asn	Ser	Glu	Lys	Arg	Lys	Ser	Leu	Cys	Lys		
				155					160					165				
15	AAG	ACA	ATC	CAG	GAC	TGT	TTC	CAA	GTT	GTC	GAC	TCC	ACC	GGG	TAT	GTG	700	
	Lys	Thr	Ile	Gln	Asp	Cys	Phe	Gln	Val	Val	Asp	Ser	Thr	Gly	Tyr	Val		
			170					175					180					
20	AGC	AAC	AGC	TAT	AAA	GAC	AGA	GCA	CAT	ATC	AGT	ATC	CTA	GGT	ACC	AAC	748	
	Ser	Asn	Ser	Tyr	Lys	Asp	Arg	Ala	His	Ile	Ser	Ile	Leu	Gly	Thr	Asn		
		185					190					195						
25	ACA	TTA	GTG	TTC	AGC	GTT	GTC	ATC	AAC	CGA	GTC	AAG	CTC	AGT	GAT	GCT	796	
	Thr	Leu	Val	Phe	Ser	Val	Val	Ile	Asn	Arg	Val	Lys	Leu	Ser	Asp	Ala		
	200					205					210					215		
30	GGG	ATG	TAT	GTC	TGC	CAG	GCT	GGG	GAC	GAT	GCC	AAA	GCC	GAT	AAA	ATC	844	
	Gly	Met	Tyr	Val	Cys	Gln	Ala	Gly	Asp	Asp	Ala	Lys	Ala	Asp	Lys	Ile		
					220					225					230			
35	AAC	ATT	GAC	CTC	CAG	GTG	CTG	GAG	CCT	GAG	CCT	GAG	CTG	GTT	TAT	GGA	892	
	Asn	Ile	Asp	Leu	Gln	Val	Leu	Glu	Pro	Glu	Pro	Glu	Leu	Val	Tyr	Gly		
				235					240					245				
40	GAC	TTG	AGG	AGC	TCG	GTG	ACC	TTT	GAC	TGT	TCC	CTG	GGC	CCC	GAG	GTG	940	
	Asp	Leu	Arg	Ser	Ser	Val	Thr	Phe	Asp	Cys	Ser	Leu	Gly	Pro	Glu	Val		
		250						255					260					
45	GCA	AAT	GTG	CCC	AAA	TTT	CTG	TGC	CAG	AAG	AAG	AAT	GGG	GGA	GCT	TGC	988	
	Ala	Asn	Val	Pro	Lys	Phe	Leu	Cys	Gln	Lys	Lys	Asn	Gly	Gly	Ala	Cys		
		265					270					275						
50	AAT	GTA	GTC	ATC	AAC	ACG	TTG	GGG	AAG	AAG	GCT	CAG	GAC	TTC	CAG	GGC	1036	
	Asn	Val	Val	Ile	Asn	Thr	Leu	Gly	Lys	Lys	Ala	Gln	Asp	Phe	Gln	Gly		
		280				285					290					295		
55	AGG	ATC	GTG	TCC	GTG	CCC	AAG	GAC	AAT	GGT	GTC	TTC	AGT	GTG	CAC	ATT	1084	
	Arg	Ile	Val	Ser	Val	Pro	Lys	Asp	Asn	Gly	Val	Phe	Ser	Val	His	Ile		
					300					305					310			
60	ACC	AGC	CTG	AGG	AAA	GAG	GAC	GCA	GGG	CGC	TAC	GTG	TGC	GGG	GCC	CAG	1132	
	Thr	Ser	Leu	Arg	Lys	Glu	Asp	Ala	Gly	Arg	Tyr	Val	Cys	Gly	Ala	Gln		
				315					320					325				
65	CCT	GAG	GGT	GAG	CCC	CAG	GAC	GGC	TGG	CCT	GTG	CAG	GCC	TGG	CAA	CTC	1180	
	Pro	Glu	Gly	Glu	Pro	Gln	Asp	Gly	Trp	Pro	Val	Gln	Ala	Trp	Gln	Leu		
			330					335					340					
70	TTC	GTC	AAT	GAA	GAG	ACG	GCA	ATC	CCC	GCA	AGC	CCC	TCC	GTG	GTG	AAA	1228	
	Phe	Val	Asn	Glu	Glu	Thr	Ala	Ile	Pro	Ala	Ser	Pro	Ser	Val	Val	Lys		
		345					350					355						
75	GGT	GTG	AGG	GGA	GGC	TCT	GTG	ACT	GTA	TCT	TGC	CCC	TAC	AAC	CCT	AAG	1276	
	Gly	Val	Arg	Gly	Gly	Ser	Val	Thr	Val	Ser	Cys	Pro	Tyr	Asn	Pro	Lys		
						365					370					375		
80	GAT	GCC	AAC	AGC	GCG	AAG	TAC	TGG	TGT	CAC	TGG	GAA	GAG	GCT	CAA	AAC	1324	
	Asp	Ala	Asn	Ser	Ala	Lys	Tyr	Trp	Cys	His	Trp	Glu	Glu	Ala	Gln	Asn		

	380	385	390	
5	GGC CGC TGC CCG CGG CTG GTG GAG AGC CGG GGG CTG ATG AAG GAG CAG Gly Arg Cys Pro Arg Leu Val Glu Ser Arg Gly Leu Met Lys Glu Gln 395 400 405			1372
10	TAC GAG GGC AGG CTG GTG CTG CTC ACC GAG CCG GGC AAC GGC ACC TAC Tyr Glu Gly Arg Leu Val Leu Leu Thr Glu Pro Gly Asn Gly Thr Tyr 410 415 420			1420
15	ACC GTC ATC CTC AAC CAG CTC ACC GAT CAG GAC GCC GGC TTC TAC TGG Thr Val Ile Leu Asn Gln Leu Thr Asp Gln Asp Ala Gly Phe Tyr Trp 425 430 435			1468
20	TGC GTG ACC GAC GGC GAC ACG CGC TGG ATC TCC ACA GTG GAG CTC AAG Cys Val Thr Asp Gly Asp Thr Arg Trp Ile Ser Thr Val Glu Leu Lys 440 445 450 455			1516
25	GTT GTC CAA GGA GAA CCA AGC CTC AAG GTA CCC AAG AAC GTC ACG GCT Val Val Gln Gly Glu Pro Ser Leu Lys Val Pro Lys Asn Val Thr Ala 460 465 470			1564
30	TGG CTG GGA GAG CCC TTA AAG CTC TCC TGC CAC TTC CCC TGC AAA TTC Trp Leu Gly Glu Pro Leu Lys Leu Ser Cys His Phe Pro Cys Lys Phe 475 480 485			1612
35	TAC TCC TTT GAG AAG TAC TGG TGT AAG TGG AGC AAC AGA GGC TGC AGC Tyr Ser Phe Glu Lys Tyr Trp Cys Lys Trp Ser Asn Arg Gly Cys Ser 490 495 500			1660
40	GCC CTG CCC ACC CAG AAC GAC GGC CCC AGC CAG GCC TTT GTG AGC TGC Ala Leu Pro Thr Gln Asn Asp Gly Pro Ser Gln Ala Phe Val Ser Cys 505 510 515			1708
45	GAC CAG AAC AGC CAG GTC GTC TCC CTG AAC CTG GAC ACA GTC ACC AAG Asp Gln Asn Ser Gln Val Ser Leu Asn Leu Asp Thr Val Thr Lys 520 525 530 535			1756
50	GAG GAT GAA GGC TGG TAC TGG TGT GGA GTG AAG GAA GGC CCC CGA TAC Glu Asp Glu Gly Tyr Trp Cys Gly Val Lys Glu Gly Pro Arg Tyr 540 545 550			1804
55	GGG GAG ACG GCG GCT GTC TAC GTG GCA GTG GAG AGC AGG GTG AAG GGG Gly Glu Thr Ala Ala Val Tyr Val Ala Val Glu Ser Arg Val Lys Gly 555 560 565			1852
60	TCC CAA GGC GCC AAG CAA GTG AAA GCT GCC CCT GCG GGG GCG GCA ATA Ser Gln Gly Ala Lys Gln Val Lys Ala Ala Pro Ala Gly Ala Ala Ile 570 575 580			1900
65	CAG TCG AGG GCC GGG GAG ATC CAG AAC AAA GCC CTT CTG GAC CCC AGC Gln Ser Arg Ala Gly Glu Ile Gln Asn Lys Ala Leu Leu Asp Pro Ser 585 590 595			1948
70	TTT TTC GCA AAG GAA AGT GTG AAG GAC GCT GCT GGT GGA CCC GGA GCA Phe Phe Ala Lys Glu Ser Val Lys Asp Ala Ala Gly Gly Pro Gly Ala 600 605 610 615			1996
75	CCT GCA GAT CCT GGC CGC CCT ACA GGA TAC AGC GGG AGC TCC AAA GCA Pro Ala Asp Pro Gly Arg Pro Thr Gly Tyr Ser Gly Ser Ser Lys Ala 620 625 630			2044
80	CTG GTC TCC ACC CTG GTG CCC CTG GCC CTG GTC CTG GTC GCA GGG GTC Leu Val Ser Thr Leu Val Pro Leu Ala Leu Val Leu Val Ala Gly Val 635 640 645			2092

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	GTG GCG ATC GGG GTG GTC CGA GCC CGG CAC AGG AAG AAC GTC GAC CGG	2140
	Val Ala Ile Gly Val Val Arg Ala Arg His Arg Lys Asn Val Asp Arg	
	650 655 660	
5	ATT TCA ATC AGG AGC TAC CGG ACA GAT ATC AGC ATG TCA GAC TTT GAG	2188
	Ile Ser Ile Arg Ser Tyr Arg Thr Asp Ile Ser Met Ser Asp Phe Glu	
	665 670 675	
10	AAC TCC AGG GAT TTT GAA GGA CGT GAC AAC ATG GGA GCC TCT CCA GAG	2236
	Asn Ser Arg Asp Phe Glu Gly Arg Asp Asn Met Gly Ala Ser Pro Glu	
	680 685 690 695	
15	GCC CAA GAG ACG TCT CTC GGA GGG AAG GAC GAG TTT GCC ACC ACT ACC	2284
	Ala Gln Glu Thr Ser Leu Gly Gly Lys Asp Glu Phe Ala Thr Thr Thr	
	700 705 710	
20	GAG GAC ACC GTG GAG AGC AAA GAA CCC AAG AAG GCA AAG AGG TCG TCC	2332
	Glu Asp Thr Val Glu Ser Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser	
	715 720 725	
25	AAG GAG GAA GCC GAC GAG GCC TTC ACC ACC TTC CTC CTC CAG GCC AAA	2380
	Lys Glu Glu Ala Asp Glu Ala Phe Thr Thr Phe Leu Leu Gln Ala Lys	
	730 735 740	
30	AAC CTG GCC TCC GCC GCA ACC CAG AAC GGC CCG ACA GAA GCC TAG ACGGAG	2431
	Asn Leu Ala Ser Ala Ala Thr Gln Asn Gly Pro Thr Glu Ala	
	745 750 755	
35	CCCTGGGCGC CCCTTCCCTC CGCACGTGGC AATCACGCTC CGAATCACGC TGATCCTCAG	2491
	GGCCCTCAGC TCGGGGGGCT CCACTGCCTG CACTCACACC CCGCCTAGGC TTCTCCTGTC	2551
	TGTCCTCAGA GGGTGTGCTG GTTCCTTCTT GGTGGCATCC AAGCCTGGCT TACTTGTTCC	2611
40	TATTGGGGGT GAGGTGGTAC GAGGAGTTCC CACCTGCAGC TTATTCGAAC GAGAGAACTA	2671
	AAGGTGTGGA GGAGAATTAA GATCGCAGAG GGGCCTCTCA GAAAGAAAAG GAGTGGGTGG	2731
	GGAGACAACC GCAGAAAGGG GGCCATTAG CAGCTTCCCTG TCCCCTTATT TGGGGATGTC	2791
45	AGTGAATCC TCCCTTCCAC CCCATCTCTG CACCTCTCCA TCCCCACTCC ATTCCATCTT	2851
	CTCTTCTTCT TTCCCTCATT AAAAATGTGC ATTTGGTTAC TCACTAGATT CCAGGGACTC	2911
50	TGCTAGACAC TGGGATAGGT AGGCCGCAAT CCCAGGCGGC AGCCTTCCGC AAACATCAAG	2971
	GAGCCCCTGG AGCCCACAGC ATCTCTTCAC GTGTACACTC ACTGACCTCT GCCTCTGCTG	3031
	GGAGAAATCA TAAAGGGTCT GCAGCCCTGA GGCCTTAGGG ATTATGTAAC ACAGGCATAC	3091
55	ACACAAGGCA CCATCAACAC ATTCTTACCA TTTCACAGGT GAGAAAGCCG AGGTCCTGAG	3151
	AGGTGGAGAG GTTTGCTCAG AGTCAGCAAG TGAGATGTAC GAGTCTCAAG CTAAAGATTT	3211
60	GACACCTGCT GTCCCTACAG GAGGGCCTCC TCTCTCCAGA TGAGACAGCA TTCCATAGGA	3271
	AGGAGAAGAA AAATGTAAAT AAGACTGGTC TTTCACAGGC CCCACATCAG GGAAGATACC	3331
	CCTTTCCCTG TCTGTCACTC ACAGAGACCT AATAGGATAA GAGAATGGTC AACACTCAAA	3391
	CCCCGAATG TGAAGAGTTC TAAGTGGAAG GGGAGGAAAA AGGGGGGATT TGATGGTGCC	3451
	AGGGAGGGGC TGATCTCCAA AGAACTAAGG TTTAAGTTTT TTTGTTTTTT TTTTCTCTC	3511
65	TTCTAAGCTC TGCACTTCAA CTAGCATCTA TGAGCTGGCA CTGCTAACA AATCAAAAAT	3571

CCCTGGGCGC CCCTTCCCTC CGCACGTGGC AATCACGCTC CGAATCACGC TGATCCTCAG

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(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 757 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear
DESCRIPTION: Bovine Polyimmunoglobulin Receptor

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

	Met 1	Ser	Arg	Leu 5	Phe	Leu	Ala	Cys	Leu 10	Ala	Ile	Phe	Pro	Val 15	Val	
20	Ser	Met	Lys 20	Ser	Pro	Ile	Phe	Gly	Pro 25	Glu	Glu	Val	Ser	Ser 30	Val	Glu
	Gly	Arg	Ser 35	Val	Ser	Ile	Lys	Cys 40	Tyr	Tyr	Pro	Pro	Thr 45	Ser	Val	Asn
25	Arg	His 50	Thr	Arg	Lys	Tyr	Trp 55	Cys	Arg	Gln	Gly	Ala 60	Gln	Gly	Arg	Cys
	Thr 65	Thr	Leu	Ile	Ser	Ser 70	Glu	Gly	Tyr	Val	Ser 75	Asp	Asp	Tyr	Val	Gly 80
30	Arg	Ala	Asn	Leu 85	Thr	Asn	Phe	Pro	Glu	Ser 90	Gly	Thr	Phe	Val	Val 95	Asp
35	Ile	Ser	His 100	Leu	Thr	His	Lys	Asp	Ser 105	Gly	Arg	Tyr	Lys	Cys 110	Gly	Leu
	Gly	Ile	Ser 115	Ser	Arg	Gly	Leu	Asn 120	Phe	Asp	Val	Ser	Leu 125	Glu	Val	Ser
40	Gln	Asp 130	Pro	Ala	Gln	Ala	Ser 135	His	Ala	His	Val	Tyr 140	Thr	Ile	Asp	Leu
	Gly 145	Arg	Thr	Val	Thr	Ile 150	Asn	Cys	Pro	Phe	Thr 155	Arg	Ala	Asn	Ser	Glu 160
45	Lys	Arg	Lys	Ser	Leu 165	Cys	Lys	Lys	Thr	Ile 170	Gln	Asp	Cys	Phe	Gln 175	Val
50	Val	Asp	Ser 180	Thr	Gly	Tyr	Val	Ser	Asn 185	Ser	Tyr	Lys	Asp	Arg 190	Ala	His
	Ile	Ser	Ile 195	Leu	Gly	Thr	Asn	Thr 200	Leu	Val	Phe	Ser	Val 205	Val	Ile	Asn
55	Arg	Val 210	Lys	Leu	Ser	Asp	Ala 215	Gly	Met	Tyr	Val	Cys 220	Gln	Ala	Gly	Asp
	Asp 225	Ala	Lys	Ala	Asp	Lys 230	Ile	Asn	Ile	Asp	Leu 235	Gln	Val	Leu	Glu	Pro 240
60	Glu	Pro	Glu	Leu 245	Val	Tyr	Gly	Asp	Leu	Arg 250	Ser	Ser	Val	Thr	Phe 255	Asp
65	Cys	Ser	Leu 260	Gly	Pro	Glu	Val	Ala	Asn 265	Val	Pro	Lys	Phe	Leu 270	Cys	Gln

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Tyr Ser Gly Ser Ser Lys Ala Leu Val Ser Thr Leu Val Pro Leu Ala
 625 630 635 640
 5 Leu Val Leu Val Ala Gly Val Val Ala Ile Gly Val Val Arg Ala Arg
 645 650 655
 His Arg Lys Asn Val Asp Arg Ile Ser Ile Arg Ser Tyr Arg Thr Asp
 660 665 670
 10 Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Asp Phe Glu Gly Arg Asp
 675 680 685
 Asn Met Gly Ala Ser Pro Glu Ala Gln Glu Thr Ser Leu Gly Gly Lys
 690 695 700
 15 Asp Glu Phe Ala Thr Thr Thr Glu Asp Thr Val Glu Ser Lys Glu Pro
 705 710 715 720
 20 Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Glu Ala Phe Thr
 725 730 735
 Thr Phe Leu Leu Gln Ala Lys Asn Leu Ala Ser Ala Ala Thr Gln Asn
 740 745 750
 25 Gly Pro Thr Glu Ala
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(2) INFORMATION FOR SEQ ID NO: 7:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3095 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 DESCRIPTION: Mouse Polyimmunoglobulin Receptor

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 85....2400
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCACCTGGAG AGAAGGAAGT AGCTAAAACA TTTCATACA AGAAGCCAAC CTGAGCGGCA 60
 50 CAGCCCCCCT GGAAGCCACA AGCA ATG AGG CTC TAC TTG TTC ACG CTC TTG 111
 Met Arg Leu Tyr Leu Phe Thr Leu Leu
 1 5
 55 GTA ACT GTC TTT TCA GGG GTC TCC ACA AAA AGC CCC ATA TTT GGT CCC 159
 Val Thr Val Phe Ser Gly Val Ser Thr Lys Ser Pro Ile Phe Gly Pro
 10 15 20 25
 60 CAG GAG GTG AGT AGT ATA GAA GGC GAC TCT GTT TCC ATC ACG TGC TAC 207
 Gln Glu Val Ser Ser Ile Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
 30 35 40
 TAC CCA GAC ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA 255
 Tyr Pro Asp Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg
 45 50 55
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	CAA GGA GCC AGC GGC ATG TGC ACA ACG CTC ATC TCT TCA AAT GGC TAC	303
	Gln Gly Ala Ser Gly Met Cys Thr Leu Ile Ser Ser Asn Gly Tyr	
	60 65 70	
5	CTC TCC AAG GAG TAT TCA GGC AGA GCC AAC CTC ATC AAC TTC CCA GAG	351
	Leu Ser Lys Glu Tyr Ser Gly Arg Ala Asn Leu Ile Asn Phe Pro Glu	
	75 80 85	
10	AAC AAC ACA TTT GTG ATT AAC ATT GAG CAG CTC ACC CAG GAC GAC ACT	399
	Asn Asn Thr Phe Val Ile Asn Ile Glu Gln Leu Thr Gln Asp Asp Thr	
	90 95 100 105	
15	GGG AGC TAC AAG TGT GGC CTG GGT ACC AGT AAC CGA GGC CTG TCC TTC	447
	Gly Ser Tyr Lys Cys Gly Leu Gly Thr Ser Asn Arg Gly Leu Ser Phe	
	110 115 120	
20	GAT GTC AGC CTG GAG GTC AGC CAG GTT CCT GAG TTG CCG AGT GAC ACC	495
	Asp Val Ser Leu Glu Val Ser Gln Val Pro Glu Leu Pro Ser Asp Thr	
	125 130 135	
25	CAC GTC TAC ACA AAG GAC ATA GGC AGA AAT GTG ACC ATT GAA TGC CCT	543
	His Val Tyr Thr Lys Asp Ile Gly Arg Asn Val Thr Ile Glu Cys Pro	
	140 145 150	
30	TTC AAA AGG GAG AAT GTT CCC AGC AAG AAA TCC CTG TGT AAG AAG ACA	591
	Phe Lys Arg Glu Asn Val Pro Ser Lys Lys Ser Leu Cys Lys Lys Thr	
	155 160 165	
35	AAC CAG TCC TGC GAA CTT GTC ATT GAC TCT ACT GAG AAG GTG AAC CCC	639
	Asn Gln Ser Cys Glu Leu Val Ile Asp Ser Thr Glu Lys Val Asn Pro	
	170 175 180 185	
40	AGC TAT ATA GGC AGA GCA AAA CTT TTT ATG AAA GGG ACC GAC CTA ACT	687
	Ser Tyr Ile Gly Arg Ala Lys Leu Phe Met Lys Gly Thr Asp Leu Thr	
	190 195 200	
45	GTA TTC TAT GTC AAC ATT AGT CAC CTA ACG CAC AAT GAT GCT GGG CTG	735
	Val Phe Tyr Val Asn Ile Ser His Leu Thr His Asn Asp Ala Gly Leu	
	205 210 215	
50	TAC ATC TGC CAA GCT GGA GAA GGT CCT AGT GCT GAT AAG AAG AAT GTT	783
	Tyr Ile Cys Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Lys Asn Val	
	220 225 230	
55	GAC CTC CAG GTG CTA GCG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG	831
	Asp Leu Gln Val Leu Ala Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu	
	235 240 245	
60	AGG TCC TCA GTG ACT TTT GAA TGT GAC CTG GGC CGT GAG GTG GCA AAC	879
	Arg Ser Ser Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn	
	250 255 260 265	
65	GAG GCC AAA TAT CTG TGC CGG ATG AAT AAG GAA ACC TGT GAT GTG ATC	927
	Glu Ala Lys Tyr Leu Cys Arg Met Asn Lys Glu Thr Cys Asp Val Ile	
	270 275 280	
70	ATT AAC ACC CTG GGG AAG AGG GAT CCA GAC TTT GAG GGC AGG ATC CTG	975
	Ile Asn Thr Leu Gly Lys Arg Asp Pro Asp Phe Glu Gly Arg Ile Leu	
	285 290 295	
75	ATA ACC CCC AAG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC	1023
	Ile Thr Pro Lys Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly	
	300 305 310	
80	CTG AGG AAG GAG GAT GCA GGG CAC TAC CAG TGT GGA GCC CAC AGT TCT	1071
	Leu Arg Lys Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser	

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

	315	320	325	
5	GGT TTG CCT CAA GAA GGC TGG CCC ATC CAG ACT TGG CAA CTC TTT GTC Gly Leu Pro Gln Glu Gly Trp Pro Ile Gln Thr Trp Gln Leu Phe Val 330 335 340 345	1119		
10	AAT GAA GAG TCT ACC ATT CCC AAT CGT CGC TCT GTT GTG AAG GGA GTC Asn Glu Glu Ser Thr Ile Pro Asn Arg Ser Val Val Lys Gly Val 350 355 360	1167		
15	ACA GGA GGC TCT GTG GCC ATC GCC TGT CCC TAT AAC CCC AAG GAA AGC Thr Gly Gly Ser Val Ala Ile Ala Cys Pro Tyr Asn Pro Lys Glu Ser 365 370 375	1215		
20	AGC AGC CTC AAG TAC TGG TGT CGC TGG GAA GGG GAC GGA AAT GGA CAT Ser Ser Leu Lys Tyr Trp Cys Arg Trp Glu Gly Asp Gly Asn Gly His 380 385 390	1263		
25	TGC CCC GCG CTT GTG GGG ACC CAG GCC CAG GTG CAA GAA GAG TAT GAA Cys Pro Ala Leu Val Gly Thr Gln Ala Gln Val Gln Glu Glu Tyr Glu 395 400 405	1311		
30	GGC CGA CTG GCA CTG TTT GAT CAG CCA GGC AAT GGT ACT TAC ACT GTC Gly Arg Leu Ala Leu Phe Asp Gln Pro Gly Asn Gly Thr Tyr Thr Val 410 415 420 425	1359		
35	ATC CTC AAC CAG CTC ACC ACC GAG GAT GCT GGC TTC TAT TGG TGT CTT Ile Leu Asn Gln Leu Thr Thr Glu Asp Ala Gly Phe Tyr Trp Cys Leu 430 435 440	1407		
40	ACC AAT GGT GAC TCT CGC TGG AGA ACC ACA ATA GAA CTC CAG GTT GCC Thr Asn Gly Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala 445 450 455	1455		
45	GAA GCT ACA AGG GAG CCA AAC CTT GAG GTG ACG CCA CAG AAC GCA ACA Glu Ala Thr Arg Glu Pro Asn Leu Glu Val Thr Pro Gln Asn Ala Thr 460 465 470	1503		
50	GCA GTA CTA GGA GAG ACC TTC ACC GTT TCC TGC CAC TAT CCG TGC AAA Ala Val Leu Gly Glu Thr Phe Thr Val Ser Cys His Tyr Pro Cys Lys 475 480 485	1551		
55	TTC TAC TCC CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC AAG GGT TGC Phe Tyr Ser Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Lys Gly Cys 490 495 500 505	1599		
60	CAC ATC CTG CCA AGC CAT GAC GAA GGT GCC CGC CAA TCT TCT GTG AGC His Ile Leu Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser 510 515 520	1647		
65	TGC GAC CAG AGC AGC CAG CTG GTC TCC ATG ACC CTG AAC CCG GTC AGT Cys Asp Gln Ser Ser Gln Leu Val Ser Met Thr Leu Asn Pro Val Ser 525 530 535	1695		
70	AAG GAA GAT GAA GGC TGG TAC TGG TGT GGG GTA AAG CAA GGC CAG ACC Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Gln Gly Gln Thr 540 545 550	1743		
75	TAT GGA GAA ACT ACC GCC ATC TAT ATA GCA GTT GAA GAG AGG ACC AGA Tyr Gly Glu Thr Thr Ala Ile Tyr Ile Ala Val Glu Glu Arg Thr Arg 555 560 565	1791		
80	GGG TCA TCC CAT GTC AAC CCA ACA GAT GCA AAT GCA CGT GCC AAA GTC Gly Ser Ser His Val Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Val 570 575 580 585	1839		

	GCT CTG GAA GAA GAG GTA GTG GAC TCC TCC ATC AGT GAA AAA GAG AAC Ala Leu Glu Glu Glu Val Val Asp Ser Ser Ile Ser Glu Lys Glu Asn 590 595 600	1887
5	AAA GCC ATT CCA AAT CCC GGG CCT TTT GCC AAC GAA AGA GAG ATA CAG Lys Ala Ile Pro Asn Pro Gly Pro Phe Ala Asn Glu Arg Glu Ile Gln 605 610 615	1935
10	AAT GTG AGA GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG GAT GCT GGC Asn Val Arg Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asp Ala Gly 620 625 630	1983
15	AGT GCT GAT GGA CAA AGC AGG AGC TCC AGC TCC AAA GTG CTG TTC TCC Ser Ala Asp Gly Gln Ser Arg Ser Ser Ser Lys Val Leu Phe Ser 635 640 645	2031
20	ACC CTG GTG CCC CTG GGT CTG GTG CTG GCA GTG GGT GCT ATA GCT GTG Thr Leu Val Pro Leu Gly Leu Val Leu Ala Val Gly Ala Ile Ala Val 650 655 660 665	2079
25	TGG GTG GCC AGA GTC CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC Trp Val Ala Arg Val Arg His Arg Lys Asn Val Asp Arg Met Ser Ile 670 675 680	2127
30	AGC AGC TAC AGG ACA GAC ATT AGC ATG GCA GAC TTC AAG AAC TCC AGA Ser Ser Tyr Arg Thr Asp Ile Ser Met Ala Asp Phe Lys Asn Ser Arg 685 690 695	2175
35	GAT TTG GGA GGC AAT GAC AAC ATG GGG GCC TCT CCA GAC ACA CAG CAA Asp Leu Gly Gly Asn Asp Asn Met Gly Ala Ser Pro Asp Thr Gln Gln 700 705 710	2223
40	ACA GTC ATC GAA GGA AAA GAT GAA ATC GTG ACT ACC ACG GAG TGC ACC Thr Val Ile Glu Gly Lys Asp Glu Ile Val Thr Thr Thr Glu Cys Thr 715 720 725	2271
45	GCT GAG CCA GAA GAA TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA Ala Glu Pro Glu Glu Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu 730 735 740 745	2319
50	GCT GAC ATG GCC TAC TCG GCA TTC CTG CTT CAG TCC AGC ACC ATA GCT Ala Asp Met Ala Tyr Ser Ala Phe Leu Leu Gln Ser Ser Thr Ile Ala 750 755 760	2367
55	GCA CAG GTC CAC GAT GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCCACCC Ala Gln Val His Asp Gly Pro Gln Glu Ala 765 770	2420
60	TTGCCTGTGA CAATCAACTT GAGAATCACA CTGATCCGCT CGCAGCCCAC ACTCACCCAT CACCTCCGCT CTTCCCTCCT GTCCTCAGAG GTGTGCTGGT TCCTTCCTCG GCCATGGAAG CCTGGCCTAG TTACGCCTGT TTAGGAGAGA GTGTGAGGCG TTCTTTTCTC TATGAAGAGA	2480 2540 2600
65	GTGAGGTGGA AATGAGGAGG AGGTGAACCT GAGAGACATC TCTGGAGGAA GAGGGTTGAG AATAGGGGCT CGTTTCAGGA GAAAAGGCCA TTTGAATCTT CTTTATAACC ATATGATAGG ATGTCAGCGT AACTCTTCTC TCCTCCATCT CTCCTTTCCT ATCCTCTTGA TTCAAACAAC ACATCTGAGA ACTCACTAGG CTTCAGTGCC TACTAAATGC TGAGAGCCAG GCCACAATCT TTCTATAAAT ATTACTGGAA GAGATGCCAT CTCCTCCCAG ATTCTGTCTT TTCATTAAGA TAAGACATCA TTACCAGGCA TACCTCCTGC CTCTGTGCCT CATAGGCATA CACAAGCCAT	2660 2720 2780 2840 2900 2960

AAGGGCATCA TGATTTTCAG ATGAGAAGAG ATGTTTCTCA AGAGTGCCTA GTGAGATAGA 3020
 CTAGCGTCAA ACCAGATGTG GCAACTCCTG GCTCTTGGCC TACGATCTGT CTTCAAGAAA 3080
 5 AAAAAAAAAA AAAAA 3095

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 771 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Mouse Polyimmunoglobulin Receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Arg Leu Tyr Leu Phe Thr Leu Leu Val Thr Val Phe Ser Gly Val
 1 5 10 15
 Ser Thr Lys Ser Pro Ile Phe Gly Pro Gln Glu Val Ser Ser Ile Glu
 20 25 30
 Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
 35 40 45
 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Ser Gly Met Cys
 50 55 60
 Thr Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
 65 70 75 80
 Arg Ala Asn Leu Ile Asn Phe Pro Glu Asn Asn Thr Phe Val Ile Asn
 85 90 95
 Ile Glu Gln Leu Thr Gln Asp Asp Thr Gly Ser Tyr Lys Cys Gly Leu
 100 105 110
 Gly Thr Ser Asn Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
 115 120 125
 Gln Val Pro Glu Leu Pro Ser Asp Thr His Val Tyr Thr Lys Asp Ile
 130 135 140
 Gly Arg Asn Val Thr Ile Glu Cys Pro Phe Lys Arg Glu Asn Val Pro
 145 150 155 160
 Ser Lys Lys Ser Leu Cys Lys Lys Thr Asn Gln Ser Cys Glu Leu Val
 165 170 175
 Ile Asp Ser Thr Glu Lys Val Asn Pro Ser Tyr Ile Gly Arg Ala Lys
 180 185 190
 Leu Phe Met Lys Gly Thr Asp Leu Thr Val Phe Tyr Val Asn Ile Ser
 195 200 205
 His Leu Thr His Asn Asp Ala Gly Leu Tyr Ile Cys Gln Ala Gly Glu
 210 215 220
 Gly Pro Ser Ala Asp Lys Lys Asn Val Asp Leu Gln Val Leu Ala Pro
 225 230 235 240
 Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu

	245	250	255
	Cys Asp Leu Gly Arg Glu Val Ala Asn Glu Ala Lys Tyr Leu Cys Arg 260 265 270		
5	Met Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg 275 280 285		
10	Asp Pro Asp Phe Glu Gly Arg Ile Leu Ile Thr Pro Lys Asp Asp Asn 290 295 300		
	Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly 305 310 315 320		
15	His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp 325 330 335		
	Pro Ile Gln Thr Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro 340 345 350		
20	Asn Arg Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile 355 360 365		
	Ala Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys 370 375 380		
25	Arg Trp Glu Gly Asp Gly Asn Gly His Cys Pro Ala Leu Val Gly Thr 385 390 395 400		
30	Gln Ala Gln Val Gln Glu Glu Tyr Glu Gly Arg Leu Ala Leu Phe Asp 405 410 415		
	Gln Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr 420 425 430		
35	Glu Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Ser Arg Trp 435 440 445		
40	Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Arg Glu Pro Asn 450 455 460		
	Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Leu Gly Glu Thr Phe 465 470 475 480		
45	Thr Val Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr 485 490 495		
	Trp Cys Lys Trp Ser Asn Lys Gly Cys His Ile Leu Pro Ser His Asp 500 505 510		
50	Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Leu 515 520 525		
55	Val Ser Met Thr Leu Asn Pro Val Ser Lys Glu Asp Glu Gly Trp Tyr 530 535 540		
	Trp Cys Gly Val Lys Gln Gly Gln Thr Tyr Gly Glu Thr Thr Ala Ile 545 550 555 560		
60	Tyr Ile Ala Val Glu Glu Arg Thr Arg Gly Ser Ser His Val Asn Pro 565 570 575		
	Thr Asp Ala Asn Ala Arg Ala Lys Val Ala Leu Glu Glu Glu Val Val 580 585 590		
65	Asp Ser Ser Ile Ser Glu Lys Glu Asn Lys Ala Ile Pro Asn Pro Gly		

595 600 605

Pro Phe Ala Asn Glu Arg Glu Ile Gln Asn Val Arg Asp Gln Ala Gln
 610 615 620

5 Glu Asn Arg Ala Ser Gly Asp Ala Gly Ser Ala Asp Gly Gln Ser Arg
 625 630 635 640

10 Ser Ser Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu
 645 650 655

Val Leu Ala Val Gly Ala Ile Ala Val Trp Val Ala Arg Val Arg His
 660 665 670

15 Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile
 675 680 685

Ser Met Ala Asp Phe Lys Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn
 690 695 700

20 Met Gly Ala Ser Pro Asp Thr Gln Gln Thr Val Ile Glu Gly Lys Asp
 705 710 715 720

Glu Ile Val Thr Thr Thr Glu Cys Thr Ala Glu Pro Glu Glu Ser Lys
 725 730 735

25 Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala
 740 745 750

30 Phe Leu Leu Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro
 755 760 765

Gln Glu Ala
 770

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(2) INFORMATION FOR SEQ ID NO: 9:

40 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 3269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 45 DESCRIPTION: Rat Polyimmunoglobulin Receptor

(ix) FEATURE:

50 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 74....2383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

55 GGCAACGAAG GTACCATGGA TCTTATACAA GAAGTGAACC AACATGCCGC AACCTCCTTG 60

GAAGCCACAA GCG ATG AGG CTC TCC TTG TTC GCC CTC TTG GTA ACT GTC 109
 Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val
 1 5 10

60 TTC TCA GGG GTC TCC ACA CAA AGC CCC ATA TTT GGT CCC CAG GAT GTG 157
 Phe Ser Gly Val Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val
 15 20 25

65 AGT AGT ATT GAA GGT AAC TCG GTC TCC ATC ACG TGC TAC TAC CCA GAC 205
 Ser Ser Ile Glu Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp

	30	35	40	
5	ACC Thr 45	TCT Ser 50	GTC Val 55	AAC Asn 60
10	AAC Asn 65	GGC Gly 70	TAC Tyr 75	CGG Arg 80
15	GAG Glu 85	TAT Tyr 90	TCA Ser 95	ACC Thr 100
20	TTT Phe 105	GTG Val 110	ATT Ile 115	AAC Asn 120
25	AAG Lys 125	TGT Cys 130	GGT Gly 135	CTG Leu 140
30	ACA Thr 145	GAG Glu 150	GTC Val 155	AGC Ser 160
35	GGG Gly 165	AAT Asn 170	GCT Ala 175	CAT His 180
40	TGC Cys 185	GAA Glu 190	GTT Val 195	ATC Ile 200
45	GAC Asp 205	GAA Glu 210	GTT Val 215	ATC Ile 220
50	CAA Gln 225	GCT Ala 230	GGA Gly 235	CTG Leu 240
55	GTG Val 245	ACT Thr 250	TTT Phe 255	GAA Glu 260
60	TAT Tyr 265	CTG Leu 270	TGT Cys 275	CGG Arg 280
65	CTG Leu 285	GGG Gly 290	AAG Lys 295	AGA Arg 300

	AGG	GAT	GAC	AAT	GAC	GGC	CGC	TTC	AGT	GTG	TTG	ATC	ACA	GGC	CTG	AGG	AAG	
	Arg	Asp	Asp	Asn	Gly	Arg	Phe	Ser	Val	Leu	Ile	Thr	Gly	Leu	Arg	Lys		
					305					310						315		
5	GAG	GAT	GCA	GGG	CAC	TAC	CAG	TGT	GGA	GCG	CAC	AGT	TCT	GGT	TTG	CCT		1021
	Glu	Asp	Ala	Gly	His	Tyr	Gln	Cys	Gly	Ala	His	Ser	Ser	Gly	Leu	Pro		
				320					325					330				
10	CAA	GAA	GGC	TGG	CCC	GTC	CAG	GCT	TGG	CAA	CTC	TTT	GTC	AAT	GAA	GAG		1069
	Gln	Glu	Gly	Trp	Pro	Val	Gln	Ala	Trp	Gln	Leu	Phe	Val	Asn	Glu	Glu		
				335					340					345				
15	TCC	ACG	ATT	CCC	AAT	AGT	CGC	TCT	GTT	GTG	AAG	GGT	GTC	ACA	GGA	GGC		1117
	Ser	Thr	Ile	Pro	Asn	Ser	Arg	Ser	Val	Val	Lys	Gly	Val	Thr	Gly	Gly		
				350					355					360				
20	TCT	GTG	GCC	ATC	GTC	TGT	CCC	TAT	AAC	CCC	AAG	GAA	AGC	AGC	AGC	CTC		1165
	Ser	Val	Ala	Ile	Val	Cys	Pro	Tyr	Asn	Pro	Lys	Glu	Ser	Ser	Ser	Leu		
						370										380		
25	AAG	TAC	TGG	TGT	CAC	TGG	GAA	GCC	GAC	GAG	AAT	GGA	CGC	TGC	CCG	GTG		1213
	Lys	Tyr	Trp	Cys	His	Trp	Glu	Ala	Asp	Glu	Asn	Gly	Arg	Cys	Pro	Val		
						385										395		
30	CTC	GTG	GGG	ACC	CAG	GCC	CTG	GTG	CAA	GAA	GGA	TAT	GAA	GGC	CGA	CTG		1261
	Leu	Val	Gly	Thr	Gln	Ala	Leu	Val	Gln	Glu	Gly	Tyr	Glu	Gly	Arg	Leu		
						400										410		
35	GCA	CTG	TTC	GAT	CAG	CCG	GGC	AGT	GGC	GCC	TAC	ACT	GTC	ATC	CTC	AAC		1309
	Ala	Leu	Phe	Asp	Gln	Pro	Gly	Ser	Gly	Ala	Tyr	Thr	Val	Ile	Leu	Asn		
																425		
40	CAG	CTC	ACC	ACC	CAG	GAT	TCT	GGC	TTC	TAC	TGG	TGT	CTT	ACC	GAT	GGT		1357
	Gln	Leu	Thr	Thr	Gln	Asp	Ser	Gly	Phe	Tyr	Trp	Cys	Leu	Thr	Asp	Gly		
																440		
45	GAC	TCT	CGC	TGG	AGA	ACC	ACG	ATA	GAA	CTG	CAG	GTT	GCT	GAA	GCT	ACA		1405
	Asp	Ser	Arg	Trp	Arg	Thr	Thr	Ile	Glu	Leu	Gln	Val	Ala	Glu	Ala	Thr		
																460		
50	AAG	AAG	CCA	GAC	CTT	GAG	GTG	ACA	CCA	CAG	AAC	GCG	ACC	GCG	GTG	ATA		1453
	Lys	Lys	Pro	Asp	Leu	Glu	Val	Thr	Pro	Gln	Asn	Ala	Thr	Ala	Val	Ile		
																475		
55	GGA	GAG	ACC	TTC	ACA	ATC	TCC	TGC	CAC	TAT	CCG	TGC	AAA	TTC	TAC	TCC		1501
	Gly	Glu	Thr	Phe	Thr	Ile	Ser	Cys	His	Tyr	Pro	Cys	Lys	Phe	Tyr	Ser		
																480		
60	CAG	GAG	AAA	TAC	TGG	TGC	AAG	TGG	AGC	AAC	GAC	GGC	TGC	CAC	ATC	CTG		1549
	Gln	Glu	Lys	Tyr	Trp	Cys</												

	560	565	570	
5	CAC ATC AAC CCG ACA GAT GCA AAC GCA CGT GCA AAA GAT GCT CCA GAG His Ile Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu 575 580 585	1837		
10	GAA GAG GCA ATG GAA TCC TCT GTC AGG GAG GAT GAA AAC AAG GCC AAT Glu Glu Ala Met Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn 590 595 600	1885		
15	CTG GAC CCC AGG CTT TTT GCA GAC GAA AGA GAG ATA CAG AAT GCG GGA Leu Asp Pro Arg Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly 605 610 615 620	1933		
20	GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG AAT GCT GGC AGT GCT GGT Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly 625 630 635	1981		
25	GGA CAA AGC GGG AGC TCC AAA GTC CTA TTC TCC ACC CTG GTG CCC CTG Gly Gln Ser Gly Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu 640 645 650	2029		
30	GGT TTG GTG CTG GCA GTG GGT GCT GTG GCT GTG TGG GTG GCC AGA GTC Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val 655 660 665	2077		
35	CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC AGC AGC TAC AGG ACA Arg His Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr 670 675 680	2125		
40	GAC ATT AGC ATG GGA GAC TTC AGG AAC TCC AGG GAT TTG GGA GGC AAT Asp Ile Ser Met Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn 685 690 695 700	2173		
45	GAC AAC ATG GGC GCC ACT CCA GAC ACA CAA GAA ACA GTC CTC GAA GGA Asp Asn Met Gly Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly 705 710 715	2221		
50	AAA GAT GAA ATA GAG ACT ACC ACC GAG TGT ACC ACC GAG CCA GAG GAA Lys Asp Glu Ile Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu 720 725 730	2269		
55	TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA GCT GAC ATG GCC TAC Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr 735 740 745	2317		
60	TCA GCA TTC CTG TTT CAG TCC AGC ACA ATA GCT GCG CAG GTC CAT GAT Ser Ala Phe Leu Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp 750 755 760	2365		
65	GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCTACCC CTGCCTGTGA CAATCAACT Gly Pro Gln Glu Ala 765	2422		
70	TGAGAATCAC ATTGATCCAC TCGCAGCCCA CCCTCGCCCA TCACCCAGGC TCTTCCCTCC	2482		
75	TGTTCTCAGA GGTGTGCTGG TTCCTCCCTC AGTCGTGGAA GCCTGGCCTA CTTATGCCTG	2542		
80	TTTAGGAGAG AGCGTGAGGA GTTCTTTTTG CTGTTAAAGA GTAAGGTGGA AATGAGTTGA	2602		
85	GCCCCAAGAGG TGTCTCTGAG AGACGAGGGT TCAGAGCAGG GGCTCATTTT AGGAGGAAGA	2662		
90	GCCATTTGAA GCCTCTTTAT ACACATATGC TAGGATGTCA GGATAGCTCT TCTCCTCCAT	2722		
95	CTCTCCTTTC TTCTCTTCTT GATTGAGACA ACAGATCCGA AAACCTCACTA GGCTTCCGGT	2782		

20
(2) INFORMATION FOR SEQ ID NO: 10:

25 (A) LENGTH: 770 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear
DESCRIPTION: Rat Polyimmunoglobulin Receptor

35	Met 1	Arg	Leu	Ser	Leu 5	Phe	Ala	Leu	Leu	Val 10	Thr	Val	Phe	Ser	Gly 15	Val
	Ser	Thr	Gln	Ser 20	Pro	Ile	Phe	Gly	Pro 25	Gln	Asp	Val	Ser	Ser 30	Ile	Glu
40	Gly	Asn	Ser 35	Val	Ser	Ile	Thr	Cys 40	Tyr	Tyr	Pro	Asp	Thr 45	Ser	Val	Asn
	Arg	His 50	Thr	Arg	Lys	Tyr	Trp 55	Cys	Arg	Gln	Gly	Ala 60	Asn	Gly	Tyr	Cys
45	Ala 65	Thr	Leu	Ile	Ser	Ser 70	Asn	Gly	Tyr	Leu	Ser 75	Lys	Glu	Tyr	Ser	Gly 80
	Arg	Ala	Ser	Leu	Ile 85	Asn	Phe	Pro	Glu	Asn 90	Ser	Thr	Phe	Val	Ile 95	Asn
50	Ile	Ala	His	Leu 100	Thr	Gln	Glu	Asp	Thr 105	Gly	Ser	Tyr	Lys	Cys 110	Gly	Leu
	Gly	Thr	Thr 115	Asn	Arg	Gly	Leu	Phe 120	Phe	Asp	Val	Ser	Leu 125	Glu	Val	Ser
55	Gln	Val 130	Pro	Glu	Phe	Pro	Asn 135	Asp	Thr	His	Val	Tyr 140	Thr	Lys	Asp	Ile
60	Gly 145	Arg	Thr	Val	Thr	Ile 150	Glu	Cys	Arg	Phe	Lys 155	Glu	Gly	Asn	Ala	His 160
	Ser	Lys	Lys	Ser	Leu 165	Cys	Lys	Lys	Arg	Gly 170	Glu	Ala	Cys	Glu	Val 175	Val
65	Ile	Asp	Ser	Thr	Glu	Tyr	Val	Asp	Pro	Ser	Tyr	Lys	Asp	Arg	Ala	Ile

5.

Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp Glu Gly Trp Tyr
 530 535 540
 5 Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu Thr Thr Ala Ile
 545 550 555 560
 Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro His Ile Asn Pro
 565 570 575
 10 Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu Glu Glu Ala Met
 580 585 590
 Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn Leu Asp Pro Arg
 595 600 605
 15 Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly Asp Gln Ala Gln
 610 615 620
 Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly Gly Gln Ser Gly
 625 630 635 640
 20 Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu Val Leu
 645 650 655
 25 Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val Arg His Arg Lys
 660 665 670
 Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile Ser Met
 675 680 685
 30 Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn Met Gly
 690 695 700
 35 Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly Lys Asp Glu Ile
 705 710 715 720
 Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu Ser Lys Lys Ala
 725 730 735
 40 Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala Phe Leu
 740 745 750
 Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro Gln Glu
 755 760 765
 45 Ala

50 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Kappa

60 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 8....320

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

	CTCGAGC	GAC	ATT	GTG	ATG	ACC	CAG	TCT	CCA	GCA	ATC	ATG	TCT	GCA	TCT	49	
	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser			
	1				5					10							
5	CCA	GGG	GAG	AAG	GTC	ACC	ATA	ACC	TGC	AGT	GCC	AGC	TCA	AGT	GTA	AGT	97
	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	
	15				20						25				30		
10	TAC	ATG	CAC	TGG	TTC	CAG	CAG	AAG	CCA	GGC	ACT	TCT	CCC	AAA	CTC	TGG	145
	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Ser	Pro	Lys	Leu	Trp	
				35						40					45		
15	CTT	TAT	AGC	ACA	TCC	AAC	CTG	GCT	TCT	GGA	GTC	CCT	GCT	CGC	TTC	AGT	193
	Leu	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	
				50					55					60			
20	GGC	AGT	GGA	TCT	GGG	ACC	TCT	TAC	TCT	CTC	ACA	ATC	AGC	CGA	ATG	GAG	241
	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Met	Glu	
			65					70					75				
25	GCT	GAA	GAT	GCT	GCC	ACT	TAT	TAC	TGC	CAT	CAA	AGG	ACT	AGT	TAC	CCG	289
	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Arg	Thr	Ser	Tyr	Pro	
			80				85					90					
30	TAC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	A	TA					322
	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile						
	95					100					105						
30	(2)	INFORMATION FOR SEQ ID NO: 12:															
	(i)	SEQUENCE CHARACTERISTICS:															
35	(A)	LENGTH:	105 amino acids														
	(B)	TYPE:	amino acid														
	(C)	STRANDNESS:	single														
	(D)	TOPOLOGY:	linear														
		DESCRIPTION:	Guy's 13 Kappa														
40	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 12:															
	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	
	1				5					10					15		
45	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	
			20						25					30			
50	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Ser	Pro	Lys	Leu	Trp	Leu	Tyr	
			35					40					45				
55	Ser	Thr	Ser	Asn	Le												

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Gamma 1

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 7...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CTCGAG ATG GAA TGG ACC TGG GTT TTT CTC TTC CTC CTG TCA GGA ACT 48
 Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr
 1 5 10

20 GCA GGC GTC CAC TCT GGG GTC CAG CTT CAG CAG TCA GGA CCT GAC CTG 96
 Ala Gly Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu
 15 20 25 30

25 GTG AAA CCT GGG GCC TCA GTG AAG ATA TCC TGC AAG GCT TCT GGA TAC 144
 Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

30 ACA TTC ACT GAC TAC AAC ATA CAC TGG GTG AAG CAG AGC CGT GGA AAG 192
 Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys
 50 55 60

AGC CTT GAG TGG ATT GGA TAT ATT TAT CCT TAC AAT GGT AAT ACT TAC 240
 Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr
 35 65 70 75

TAC AAC CAG AAG TTC AAG AAC AAG GCC ACA TTG ACT GTA GAC AAT TCC 288
 Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser
 80 85 90

40 TCC ACC TCA GCC TAC ATG GAG CTC CGC AGC CTG ACA TCT GAG GAC TCT 336
 Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser
 95 100 105 110

45 GCA GTC TAT TAC TGT GCA ACC TAC TTT GAC TAC TGG GGC CAA GGC ACC 384
 Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 115 120 125

ACT CTC ACA GTC TCC TCA 402
 Thr Leu Thr Val Ser Ser
 130

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Gamma 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15
 Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
 5 20 25 30
 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu
 10 50 55 60
 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr
 15 85 90 95
 Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 20 100 105 110
 Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
 115 120 125
 Thr Val Ser Ser
 25 130

30

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACCAGATCTA TGGAATGGAC CTGGGTTTTT C 31

45

50 (2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

60

CCCAAGCTTG GTTTTGGAGA TGGTTTTCTC 30

65

